Claims to Issue in Application No. 09/365,121

1. A purified decoy probe comprising:

a first nucleotide base recognition sequence region, wherein said first region binds to an RNA polymerase; and

a second nucleotide base recognition sequence region joined directly to the 5' end of said first region or is joined to the 3' end or 5' end of said first region by a non-nucleotide linker, wherein said optionally present second region is present if said first region can be used to produce a functional double-stranded promoter sequence using a complementary oligonucleotide,

further provided that if said first region is nucleic acid which can be used to produce said functional double-stranded promoter sequence using said complementary oligonucleotide, then said decoy probe does not have a nucleic acid sequence greater than about 10 nucleotides in length joined directly to the 3' end of said first region and said decoy probe does not have a 3' end that can participate in a polymerase reaction.

2. The probe of claim 1, wherein said first region is nucleic acid, said second region is present and directly joined to the 5' end of said first region, and said probe does not have a nucleic acid sequence greater than 10 nucleotides in length joined directly to its 3' end.

3. The probe of claims 1, wherein said probe consists of 15 to 100 optionally modified nucleosides and one or more blocking groups located at the 3' terminus of said probe, wherein each of said optionally modified nucleosides independently has, a purine or pyrimidine moiety independently selected from the group consisting of inosine, uracil, adenine, guanine, thymine and cytosine; and a sugar moiety independently selected from the group consisting of deoxyribose, 2'-methoxy ribose, and ribose; and each of said optionally modified nucleosides is joined together by an internucleoside linkage independently selected from the group consisting of phosphodiester, phosphorothioate, and methylphosphonate.

4. The probe of claim 3, wherein at least 80% of said optionally modified nucleosides have a purine or pyrimidine moiety independently selected from the group consisting of adenine, guanine, thymine and cytosine, and a deoxyribose sugar moiety; and at least 80% of said internucleoside linkages joining said optionally modified nucleosides are phosphodiester.

5. The probe of claim 4, wherein said probe consists of 15 to 100 independently selected deoxyribonucleotides and one or more blocking groups located at the 3' terminus of said probe.

6. The probe of claim 3, wherein said one or more blocking groups are selected from the group consisting of phosphorothioate, alkane-diol residue, cordycepin, and an alkyl group.

7. The probe of claim 6, wherein said probe consists of 35 to 70 independently selected nucleotides, said one or more blocking groups, and said second region comprises a nucleotide base sequence at least 10 bases in length.

8. The probe of claim 7, wherein said RNA polymerase is T7 RNA polymerase.

9. The probe of claim 7, wherein said RNA polymerase is T3 RNA polymerase.

10. The probe of claim 7, wherein said RNA polymerase is SP6 RNA polymerase.

11. (Three Times Amended) A purified decoy probe comprising:

a first nucleotide base recognition sequence region, wherein said first region has at least 35% sequence similarity to an RNA polymerase promoter sequence; and

a second nucleotide base recognition sequence region joined directly to the 5' end of said first region or is joined to the 3' end or 5' end of said first region by a non-nucleotide linker, wherein said optionally present second region is present if said first region can be used to produce a functional double-stranded promoter sequence using a complementary oligonucleotide,

further provided that if said first region is nucleic acid which can be used to produce said functional double-stranded promoter sequence using said complementary oligonucleotide, then

said decoy probe does not have a nucleic acid sequence greater than about 10 nucleotides in length joined directly to the 3' end of said first region and said decoy probe does not have a 3' end that can participate in a polymerase reaction.

12. The probe of claim 11, wherein said first region is nucleic acid, said second region is present and directly joined to the 5' end of said first region, and said probe does not have a nucleic acid sequence greater than 10 nucleotides in length joined directly to its 3' end.

13. The probe of claim 11, wherein said probe consists of 15 to 100 optionally modified nucleosides and one or more blocking groups located at the 3' terminus of said probe, wherein each of said optionally modified nucleosides independently has, a purine or pyrimidine moiety independently selectedfrom the group consisting of inosine, uracil, adenine, guanine, thymine and cytosine; and a sugar moiety independently selected from the group consisting of deoxyribose, 2'-methoxy ribose, and ribose; and each of said optionally modified nucleosides is joined together by an internucleoside linkage independently selected from the group consisting of phosphodiester, phosphorothioate, and methylphosphonate.

14. The probe of claim 13, wherein at least 80% of said optionally modified nucleosides has a purine or pyrimidine moiety independently selected from the group consisting of adenine, guanine, thymine and cytosine, and a deoxyribose sugar moiety; and at least 80% of said internucleoside linkages joining said optionally modified nucleosides are phosphodiester.

15. The probe of claim 14, wherein said probe consists of 35 to 70 independently selected nucleotides, said one or more blocking groups, and said second region comprises a nucleotide base sequence at least 10 bases in length.

16. The probe of claim 13, wherein said one or more blocking groups are selected from the group consisting of phosphorothioate, alkane-diol residue, cordycepin, and an alkyl group.

17. The probe of claim 16, wherein said first region has a nucleotide base sequence similarity of at least 75% with at least one of SEQ ID Nos.1, 2, 3, 4, 5 and 6.

18. The probe of claim 17, wherein said first region has a sequence similarity of 75% to 95% with SEQ ID NO: 3.

19. A reagent mixture for use in an amplification reaction comprising an RNA polymerase and a reversible inhibitor of said polymerase, said inhibitor being a decoy probe comprising a nucleotide base recognition sequence having at least 35% sequence similarity to a promoter sequence for said RNA polymerase, wherein said reagent mixture does not contain a nucleic acid substantially complementary to said inhibitor.

20. The reagent mixture of claim 19, wherein said reagent mixture does not contain an oligonucleotide having a 3' OH available for a primer extension reaction, and said inhibitor is not a substrate in a primer extension reaction.

34. The probe of claim 1, wherein said first region is nucleic acid which can be used to produce said functional double-stranded promoter sequence using said complementary oligonucleotide, and wherein said probe does not have a nucleic acid sequence greater than about 5 nucleotides in length joined directly to the 3' end of said first region.

35. The probe of claim 1, wherein said second region is present and includes at least about 10 nucleotide base recognition groups.

36. The probe of claim 1, wherein said second region is present and includes at least about 15 nucleotide base recognition groups.

37. The probe of claim 1, wherein said second region is present and includes at least about 20 nucleotide base recognition groups.

38. The probe of claim 11, wherein said first region is nucleic acid which can be used to produce said functional double-stranded promoter sequence using said complementary oligonucleotide, and wherein said probe does not have a nucleic acid sequence greater than about 5 nucleotides in length joined directly to the 3' end of said first region.

39. The probe of claim 11, wherein said second region is present and includes at least about 10 nucleotide base recognition groups.

40. The probe of claim 11, wherein said second region is present and includes at least about 15 nucleotide base recognition groups.

41. The probe of claim 11, wherein said second region is present and includes at least about 20 nucleotide base recognition groups.

42. The reagent mixture of claim 19, wherein said first region has at least 50% sequence similarity to a promoter sequence for said RNA polymerase, wherein said promoter sequence is a T7 RNA polymerase promoter sequence, a T3 RNA polymerase promoter sequence or an SP6 RNA polymerase promoter sequence.

43. The reagent mixture of claim 19, wherein said first region has at least 75% sequence similarity to a promoter sequence for said RNA polymerase, wherein said promoter sequence is a T7 RNA polymerase promoter sequence, a T3 RNA polymerase promoter sequence or an SP6 RNA polymerase promoter sequence.

44. The reagent mixture of claim 19, wherein said first region has a sequence similarity of 75% to 95% to a promoter sequence for said RNA polymerase, wherein said promoter sequence is a T7 RNA polymerase promoter sequence, a T3 RNA polymerase promoter sequence or an SP6 RNA polymerase promoter sequence.